

Amendments To the Claims

Claim 1 (Currently amended): A method to induce homologous recombination between nucleotide sequences having homologous regions of a nucleotide sequence in within a recombination construct within in a plant, wherein said recombination construct comprises a transposon flanked by said nucleotide sequences, comprising: introducing said recombination construct to the plant, and expressing a transposase within the plant to cause excision of said transposon, so as to induce homologous recombination between said nucleotide sequences in-within said recombination construct within said plant.

Claim 2 (Currently amended): The method of claim 1, wherein the recombination construct comprises a maize Ds element as the transposon and the transposase is of maize origin.

Claim 3 (Previously presented): The method of claim 2, wherein the recombination construct further comprises direct repeats proximal to the Ds element.

Claim 4 (Previously presented): The method of claim 2, wherein the plant in which recombination is induced is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; *Arabidopsis*; and cabbage.

Claim 5 (Currently amended): A method to construct a functional gene in plants, comprising generating overlapping fragments of the gene, linking a pair of overlapping fragments with a maize Ds element, assembling a recombination construct comprising the overlapping fragments flanking the Ds element in such an order that a complete sequence is obtained when these fragments are homologously recombined, introducing said recombination construct into a plant, and making available a transposase to cause excision of the Ds element, whereby homologous recombination is induced between the overlapping fragments within the recombination construct to produce a functional gene introducing to the plant a maize recombination construct having overlapping sequences having homologous regions, which sequences, when homologously recombined, result in a functional gene, and expressing a transposase within the plant, so as to induce recombination and construction of said functional gene.

Claim 6 (Previously presented): The method of claim 5, wherein the functional gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

Claim 7 (Previously presented): The method of claim 5, wherein the plant in which recombination is induced is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; *Arabidopsis*; and cabbage.

Claim 8 (Currently amended): A method to control expression of a gene induce recombination in a plant comprising:

- 1) generating overlapping fragments of the gene sequence comprising regulatory elements;
- 2) linking a pair of overlapping fragments with a maize Ds element;
- 3) assembling a recombination construct comprising the overlapping fragments flanking the Ds element in such an order that a complete sequence is obtained when these fragments are homologously recombined;
- 4) introducing said recombination construct into a plant; and
- 5) making available a transposase to cause excision of the Ds element, whereby homologous recombination is induced between the overlapping fragments within the recombination construct to produce a complete gene sequence which is capable of expressing functional transcript in plants introducing to the plant a maize Ds element containing overlapping sequences having homologous regions to fragments of a gene, wherein said fragments together contain the complete gene; and expressing subsequently to the transformation of said Ds element a transposase within the plant, so as to induce homologous recombination and subsequent transcription of said complete gene.

Claim 9 (Previously presented): The method of claim 8, wherein the gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

Claim 10 (Original): A method of claim 9, wherein the plant in which recombination is induced is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; Arabidopsis; and cabbage.

Claims 11-17 (Cancelled)

Claim 18 (Currently amended): A recombination construct comprising a DNA molecule which can be induced to undergo homologous recombination in the presence of a maize transposase, said recombination construct comprising direct repeat sequences proximal to a Ds element and ~~an agronomically significant gene~~ internal to the direct repeats.

Claim 19 (Currently amended): A vector comprising a recombination construct comprising a DNA molecule ~~which is part of a vector, wherein said DNA molecule can be induced to undergo capable of undergoing~~ homologous recombination upon introduction of a maize transposase, wherein said DNA molecule said recombination construct comprising comprises direct repeat sequences proximal to a Ds element and ~~an~~ ~~agronomically significant gene~~ internal to the direct repeats.

Claim 20 (Currently amended): A recombination construct comprising a DNA molecule which can be induced to undergo homologous recombination in a plant upon expression of a maize transposase, wherein said recombination construct comprises direct

repeat sequences proximal to a Ds element and an agronomically significant gene internal to the direct repeats.

Claim 21 (Previously presented): The recombination construct of claim 18, which further comprises a transposase gene under control of an inducible promoter.

**Claim 22 (Canceled)**

Claim 23 (Previously presented): The recombination construct of claim 20, wherein said direct repeat sequences are in the form of overlapping sequences having homologous regions.

Claim 24 (Original): The method of claim 3, wherein the recombination construct further comprises an agronomically significant gene internal to the direct repeats.

Claim 25 (Currently amended): The method of claim 24, wherein the agronomically significant gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

Claim 26 (Previously presented): The method of claim 3, wherein the recombination construct further comprises a transposase gene under the control of an inducible promoter.

**Claim 27 (Previously presented):** The method of claim 3, wherein the transposase is Ac.

**Claim 28 (Previously presented):** The method of claim 26, wherein the transposase is Ac.

**Claim 29 (Previously presented):** The method of claim 2, wherein the plant in which recombination is induced is maize.

**Claim 30 (Previously presented):** The method of claim 2, wherein the maize Ds element comprises overlapping sequences having homologous regions, which sequences, when homologously combined, results in a functional gene.

**Claim 31 (Previously presented):** The method of claim 1, wherein the plant is a monocot.

**Claim 32 (Previously presented):** The method of claim 1, wherein the plant is a dicot.

**Claim 33 (Previously presented):** The method of claim 30, wherein the gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

Claim 34 (Previously presented): The recombination construct of claim 21, wherein the transposase is Ac.

Claim 35 (Previously presented): The recombination construct of claim 18, wherein the gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; genes useful fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

Claim 36 (Currently amended): The method of claim 21 wherein the recombination construct further comprises a transposon and direct repeats proximal to the transposon.